

SEQUENCE LISTING

<110> K. Sampath et al.

<120> METHODS FOR MAINTAINING OR RESTORING TISSUE-APPROPRIATE PHENOTYPE OF
SOFT TISSUE CELLS

<130> CIBT-P01-520

<140> 09/581,770

<141> 2000-12-29

<150> PCT/US98/26788

<151> 1998-12-16

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 1067

<212> DNA

<213> Mus musculus

<400> 1

```
tcgatcctaa aacacttaag gatatttctg taaggctgtg aaagagaaaa ccaactactt      60
acacggatgg agaccatgtt tatttctttg ggagaaaagc ctaattggga cgcttcgaga      120
tccctatagg aaattgcacc agtagtcaac tggattttta aaaggcaaag cttgaggatt      180
tttttttccc ttgaaatga atgtagcaaa cttatgtaag cacggaatag gattattagt      240
taacagtctt ttcaattata tgggaaaatg aaaactaggg gagcgtctaa ggccacttgc      300
tgacctttgt gcagctgtta agtaaagaaa gtaaaccctc cagggatact gaacagccaa      360
ctgtcataag tccaggggtgt cttgcacttg ctgtgacaag tttaaaatat ttaatatgac      420
tatacctgaa atatttaatg ctatcttttt catgcaccag cttctaagag ctttccctaa      480
aatcctgata tgcaaaagaa tataccaata ttttccccct tgccccctggc gcttgtctcc      540
caagttagca aacacttagg taagcgattt ttacagaact tttttcccta ataactgaag      600
gactaacatg atgatttaga tctatattct ccccaaaagg cgtctcatat ttttgtatat      660
taccaaatat tttcagtcaa ataacacaag aatgtatttt aaaaataaaa aggggtgaatc      720
atcattccat catgaaccaa cattggagtc agaactccta aaaggaaaac agaaaaaaaa      780
aaaaaatcat gcacagccga agctattaat atataatgga gacaaagagt ttatTTTTTca      840
atgagaataa caaggaaaaa agcctgattt tgtacgctg cccgtagga cttcccacca      900
taattagtgc ttcttgcccc tgagaggagg agcttcggct caggggaact tcatgcaata      960
agggaagaaa acagtataaa tactccaggg cagccgtggg gaaggcatta tccactgctc     1020
```

ctgggcagag gaagccagga aagctgcccc acgcatctcc cagcacc

1067

<210> 2
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> AP1 sequence A

<400> 2
 cgcttgatga ctcagccgga a

21

<210> 3
 <211> 10
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> AP1 sequence A mutation

<400> 3
 ttcctcatca

10

<210> 4
 <211> 25
 <212> PRT
 <213> Homo sapiens

<400> 4

Lys Val Glu Gln Leu Ser Pro Glu Glu Glu Glu Lys Arg Arg Ile Arg
 1 5 10 15

Arg Ile Arg Asn Lys Met Ala Ala Ala
 20 25

<210> 5
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> AP-1 consensus sequence

<400> 5
 gtgactcagc gcgga

15

<210> 6
 <211> 11
 <212> DNA

<213> Artificial Sequence

<220>
 <223> MEF-2 consensus sequence

<400> 6
 ctaaaaataa c

11

<210> 7
 <211> 1822
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (49)..(1341)
 <223>

<400> 7

```

ggtgcgggcc cggagcccgg agcccgggta ggcgctagag ccggcgcg atg cac gtg      57
                                     Met His Val
                                     1

cgc tca ctg cga gct gcg gcg ccg cac agc ttc gtg gcg ctc tgg gca      105
Arg Ser Leu Arg Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
   5                               10                               15

ccc ctg ttc ctg ctg cgc tcc gcc ctg gcc gac ttc agc ctg gac aac      153
Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
  20                               25                               30                               35

gag gtg cac tcg agc ttc atc cac cgg cgc ctc cgc agc cag gag cgg      201
Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
                               40                               45                               50

cgg gag atg cag cgc gag atc ctc tcc att ttg ggc ttg ccc cac cgc      249
Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
   55                               60                               65

ccg cgc ccg cac ctc cag ggc aag cac aac tcg gca ccc atg ttc atg      297
Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
   70                               75                               80

ctg gac ctg tac aac gcc atg gcg gtg gag gag ggc ggc ggg ccc ggc      345
Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly
   85                               90                               95

ggc cag ggc ttc tcc tac ccc tac aag gcc gtc ttc agt acc cag ggc      393
Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
  100                               105                               110                               115

ccc cct ctg gcc agc ctg caa gat agc cat ttc ctc acc gac gcc gac      441
Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp
                               120                               125                               130

atg gtc atg agc ttc gtc aac ctc gtg gaa cat gac aag gaa ttc ttc      489
Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe
                               135                               140                               145

cac cca cgc tac cac cat cga gag ttc cgg ttt gat ctt tcc aag atc      537
His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile
   150                               155                               160

cca gaa ggg gaa gct gtc acg gca gcc gaa ttc cgg atc tac aag gac      585
Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp
   165                               170                               175

```

tac atc cgg gaa cgc ttc gac aat gag acg ttc cgg atc agc gtt tat Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr 180 185 190 195	633
cag gtg ctc cag gag cac ttg ggc agg gaa tcg gat ctc ttc ctg ctc Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu 200 205 210	681
gac agc cgt acc ctc tgg gcc tcg gag gag ggc tgg ctg gtg ttt gac Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp 215 220 225	729
atc aca gcc acc agc aac cac tgg gtg gtc aat ccg cgg cac aac ctg Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu 230 235 240	777
ggc ctg cag ctc tcg gtg gag acg ctg gat ggg cag agc atc aac ccc Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro 245 250 255	825
aag ttg gcg ggc ctg att ggg cgg cac ggg ccc cag aac aag cag ccc Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro 260 265 270 275	873
ttc atg gtg gct ttc ttc aag gcc acg gag gtc cac ttc cgc agc atc Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile 280 285 290	921
cgg tcc acg ggg agc aaa cag cgc agc cag aac cgc tcc aag acg ccc Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro 295 300 305	969
aag aac cag gaa gcc ctg cgg atg gcc aac gtg gca gag aac agc agc Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser 310 315 320	1017
agc gac cag agg cag gcc tgt aag aag cac gag ctg tat gtc agc ttc Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe 325 330 335	1065
cga gac ctg ggc tgg cag gac tgg atc atc gcg cct gaa ggc tac gcc Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala 340 345 350 355	1113
gcc tac tac tgt gag ggg gag tgt gcc ttc cct ctg aac tcc tac atg Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met 360 365 370	1161
aac gcc acc aac cac gcc atc gtg cag acg ctg gtc cac ttc atc aac Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn 375 380 385	1209
ccg gaa acg gtg ccc aag ccc tgc tgt gcg ccc acg cag ctc aat gcc Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala 390 395 400	1257
atc tcc gtc ctc tac ttc gat gac agc tcc aac gtc atc ctg aag aaa Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys 405 410 415	1305

tac aga aac atg gtg gtc cgg gcc tgt ggc tgc cac tagctcctcc 1351
 Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430

gagaattcag accctttggg gccaaagtttt tctggatcct ccattgctcg ccttgccag 1411
 gaaccagcag accaactgcc ttttgtgaga ccttcccctc cctatcccca actttaaaagg 1471
 tgtgagagta ttaggaaaca tgagcagcat atggcttttg atcagttttt cagtggcagc 1531
 atccaatgaa caagatccta caagctgtgc aggcaaaacc tagcaggaaa aaaaaacaac 1591
 gcataaagaa aaatggccgg gccaggtcat tggtgggaa gtctcagcca tgcacggact 1651
 cgtttccaga ggtaattatg agcgcctacc agccaggcca cccagccgtg ggaggaaggg 1711
 ggcgtggcaa ggggtgggca cattggtgtc tgtgcgaaag gaaaattgac ccggaagttc 1771
 ctgtaataaa tgtcacaata aaacgaatga atgaaaaaaaa aaaaaaaaaa a 1822

<210> 8

<211> 431

<212> PRT

<213> Homo sapiens

<400> 8

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
 1 5 10 15

Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
 20 25 30

Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
 35 40 45

Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
 50 55 60

Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
 65 70 75 80

Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
 85 90 95

Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
 100 105 110

Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
 115 120 125

Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
 130 135 140

Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
 145 150 155 160

Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
 165 170 175

Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
 180 185 190

Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
 195 200 205

Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
 210 215 220

Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
 225 230 235 240

His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
 245 250 255

Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
 260 265 270

Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
 275 280 285

Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
 290 295 300

Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
 305 310 315 320

Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
 325 330 335

Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
 340 345 350

Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
 355 360 365

Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
 370 375 380

Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
 385 390 395 400

Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
 405 410 415

Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430